IN THE SPECIFICATION

Please amend the specification as follows. Paragraphs that are being amended are listed in their entirety; changes are indicated in the left margin with a vertical change bar. Deletions are marked by strikethrough; insertions are double underlined.

Please amend Page 17, lines 6-25 as follows:

Figs. 2A-2C1-2. Fig. 2A diagrams a selection scheme for C_H3 heterodimer using phage display vector, pRA2. Phage displaying stable C_H3 heterodimers are captured using an antibody directed to the gD flag. Fig. 2B diagrams a dicistronic operon in which C_H3 expressed from a synthetic gene is co-secreted with a second copy of C_H3 expressed from the natural gene (Ellison et al. Nucleic Acids Res. 10:4071-4079 (1982)) as a fusion protein with MI3 gene III protein. The synthetic C_H3 gene is preceded by a sequence encoding a peptide derived from herpes simplex virus glycoprotein D (gD flag, Lasky, L. A. and Dowbenko, D. J. (1984) DNA 3:23-29; Berman, P. W. et al., (1985) Science 227:1490-1492 and a cleavage (G) site for the site-specific protease, Genenase I (Carter, P. et al. (1989) Proteins: Structure, Function and Genetics 6:240-248). Fig. 2C1-2 is the nucleic acid sequence of the dicistronic operon (SEQ ID NO:1) of Fig. 2B in which the residues in the translated C_H3 genes are numbered according to the Eu system of Kabat et al. In Sequences of Proteins of Immunological Interest, 5th ed. vol. 1, pp. 688-696, NIH, Bethesda, MD (1991). Protuberance mutation T366W is shown, as are the residues targeted for randomization in the natural C_H3 gene (366, 368, and 407).